



Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 165 170 175  
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 180 185 190  
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 195 200 205  
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 210 215 220  
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 225 230 235 240  
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 245 250 255  
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 260 265 270  
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 275 280 285  
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 290 295 300  
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 305 310 315 320  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 325 330 335  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 340 345 350  
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 355 360 365  
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
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 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 385 390 395 400  
 Leu

<210> 2

<211> 283

<212> PRT

<213> HOMO SAPIENS

<400> 2

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 Pro Cys Tyr Ala Pro Ala Leu Pro Phe Cys Lys Glu Asp Glu Tyr Pro  
 35 40 45  
 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys  
 50 55 60  
 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro  
 65 70 75 80  
 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys  
 85 90 95  
 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser  
 100 105 110  
 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile  
 115 120 125  
 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser  
 130 135 140



Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe  
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 Phe Gly Ala Phe Leu Val Gly  
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 Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly  
 35 40 45  
 Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg  
 50 55 60  
 Leu Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp  
 65 70 75 80  
 Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala  
 85 90 95  
 His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu  
 100 105 110  
 Leu Trp Glu Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr  
 115 120 125  
 His Asp Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr  
 130 135 140  
 Ser Lys Val Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser  
 145 150 155 160  
 Thr Ile Thr His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu  
 165 170 175  
 Leu Glu Leu Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser  
 180 185 190  
 Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His  
 195 200 205  
 Leu Glu Ala Gly Glu Lys Val Val Val Arg Val Leu Asp Glu Arg Leu  
 210 215 220  
 Val Arg Leu Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val  
 225 230 235 240

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 agaccgacat ccatttcacg aggctgggac gaagccaccg gagacagtgc tgcagtgtgg 180  
 cccgggtggg tctgggtctc ttgctgttgc tgatgggggc tgggctggcc gtccaaggct 240  
 ggttctctct gcagctgcac tggcgtctag gagagatggc caccgcctg cctgacggac 300  
 ctgcaggctc ctgggagcag ctgatacaag agcgaaggtc tcacgaggtc aaccacgacg 360  
 cgcattctcac aggggccaac tccagcttga ccggcagcgg ggggccgctg ttatgggaga 420  
 ctgagctggg cctggccttc ctgaggggcc tcagctacca cgatggggcc cttgtggtca 480  
 ccaaagctgg ctactactac atctactcca aggtgcagct gggcggtgtg ggctgcccgc 540

tgggcctggc	cagcaccatc	acccacggcc	tctacaagcg	cacaccccgc	taccccgagg	600
agctggagct	gttggtcagc	cagcagtcac	cctgcggacg	ggccaccagc	agctcccggg	660
tctggtggga	cagcagcttc	ctgggtggtg	tggtacacct	ggaggctggg	gagaaagtgg	720
tcgtccgtgt	gctggatgaa	cgccctggttc	gactgcgtga	tggtacccgg	tcttacttcg	780
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